



STIC Search Report

Biotech-Chem Library

10/042059

File Copy
updated

STIC Database Tracking Number: 146941

TO: David Lamberston
Location: rem/2b79/2c70
Wednesday, April 13, 2005
Art Unit: 1636
Serial Number: 10/042059

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

From: Lambertson, David
Sent: Tuesday, April 05, 2005 1:43 PM
To: STIC-Biotech/ChemLib
Cc: Lambertson, David
Subject: Search Request

Search Request

Examiner's Name: David Lambertson
Examiner #: 79514
Art Unit: 1636
Room #: Remsen 02B79
Mailbox room#: Remsen 02C70
Phone: (571) 272-0771
Results Format: paper

Serial # 10/042059

Please Search:

Nucleic Acid databases for:

SEQ ID NO: 1

Including:

1. Oligo Search.

Thanks,
Dave.

1-843 N/A
LB

4/5/05

Date completed:

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

☒ Other CGN

Lambertson
10/04/2007 Page 1
Seq ID 1

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 19:04:40 / Search time 416 Seconds
(without alignments)
9924.137 Million cell updates/sec

Title: US-10-042-059B-1

Perfect score: 843
Sequence: 1 atgagcttatgaagcagca.....tctctctgctgctgctag 843

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_scs: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	100.0	843	BD266599	Nucleic a
2	843	100.0	843	AX043758	Sequence
3	843	100.0	1652	AF204738	Pichia an
4	843	100.0	1655	BD266600	Nucleic a
5	843	100.0	1655	AX043760	Sequence
6	325.2	38.6	110000	CR382131_20	Continuation (21 o
7	281.8	33.4	110000	CR382138_20	Continuation (21 o
8	270	32.0	948	AR548979	Sequence
9	256.4	30.4	110000	AB016817_01	Continuation (2 of
10	217.4	25.8	2059	YSCAR07A	M24517 Saccharomy
11	217.4	25.8	43776	SC9499X	Z49219 S.cerevisia
12	217.4	25.8	165536	SCCHRXV1	271255 S.cerevisia
13	217.2	25.8	771	AY693179	Saccharom
14	210.4	22.4	110000	CR382132_07	Continuation (8 of
15	189	18.6	869	BD178335	Transfom
16	156.4	18.6	869	AB116236	AB116236 Rosellini
17	156.4	18.6	869	AB116236	AB116236 Rosellini
18	141.8	15.6	1231	AR405512	Oryza sat
19	131.4	15.6	1231	AR404687	Sequence

20	131.4	15.6	1250	8	AK068983	Oryza sat
21	113.6	13.5	3167	8	AF133241	Emeritcell
22	111.2	12.3	1223	6	AR404686	Sequence
23	110	13.0	1000	8	LA7356	Lycopersico
24	107.6	12.8	951	8	BT005306	Arabidops
25	107.6	12.8	1143	8	AK117860	Arabidops
26	104.4	12.4	1217	6	AR236635	Sequence
27	104.4	12.4	1217	6	AR236641	Sequence
28	104.4	12.4	1217	6	AX464576	Sequence
29	104.4	12.4	1217	6	AX464582	Sequence
30	104.4	12.4	1217	8	AF131219	Arabidops
31	100.6	11.9	110000	2	AP006499_05	Continuation (6 of
32	99.8	11.8	1020	6	AR404688	Sequence
33	97.4	11.6	798	6	AX506277	Sequence
34	97.4	11.6	829	8	AY133840	Arabidops
35	97.4	11.6	933	6	AX343935	Sequence
36	97.4	11.6	1006	6	AR236634	Sequence
37	97.4	11.6	1006	6	AR236640	Sequence
38	97.4	11.6	1006	6	AX343933	Sequence
39	97.4	11.6	1006	6	AX464575	Sequence
40	97.4	11.6	1006	6	AX464581	Sequence
41	97.4	11.6	1006	8	LA7355	Arabidops
42	97.4	11.6	1055	8	AY065238	Arabidops
43	93.6	11.1	1005	6	AX506042	Sequence
44	93.6	11.1	1207	6	AR236633	Sequence
45	93.6	11.1	1207	6	AR236639	Sequence

ALIGNMENTS

RESULT 1
BD266599
LOCUS
DEFINITION
Nucleic acid molecule, containing a nucleic acid which codes for a polypeptide with chorismate mutase activity.

ACCESSION
BD266599
VERSION
JP 2002542788-A/1.

KEYWORDS
SOURCE
ORGANISM
Pichia angusta

REFERENCE
Gellissen, G., Braus, G., Pries, R., Krappmann, S. and Strasser, A.W.
Nucleic acid molecule, containing a nucleic acid which codes for a polypeptide with chorismate mutase activity

JOURNAL
RHEIN-BIOTECH GESELLSCHAFT FUER NEUE BIOTECHNOLOGISCHE PROZESSE UND
PRODUKTE MBH
OS Hansenula polymorpha (yeast)
PN JP 2002542788-A/1
PD 17-DEC-2002
PF 27-APR-2000 JP 2000614405
PR 27-APR-1999 DE 199 19 124.7
PI GERD GELLISSEN, GERHARD BRAUS, RALPH PRIES, SVEN KRAPPMANN, PI
ALEXANDER W STRASSER
PC C12N15/09, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
PC C12N9/90, C12N15/00,
PC C12N5/00
CC Nucleic acid molecule, containing a nucleic acid which codes
for a
CC polypeptide with chorismate mutase activity
FH key
FT source
FT 1. 843
Location/Qualifiers
Location/Qualifiers
1. 843
/organism="Hansenula polymorpha (yeast)"
/organism="Pichia angusta"
/mol_type="genomic DNA"
/db_xref="taxon:4905"

FEATURES

source

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM nucleic - nucleic search, using ew model

Run on: April 9, 2005, 18:36:30 ; Search time 586 Seconds
(without alignments)
8515.942 Million cell updates/sec

Title: US-10-042-059B-1

Perfect score: 843
Sequence: 1 atgcagcttatgaagccagca.....tctcctcgtcgttactag 843

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2003ds:*
11: geneseqn2003es:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	843	100.0	843	3 AAC81949	AAC81949 H. polymo
2	843	100.0	1655	3 AAC81950	AAC81950 H. polymo
3	270	32.0	807	12 ADP98547	ADP98547 C. albica
4	182.8	21.7	801	13 ADR85510	ADR85510 Aspergill
5	156.4	18.6	869	8 AAL50282	AAL50282 M. sterili
6	141.2	16.7	989	13 ADR84923	ADR84923 Aspergill
7	141.2	16.7	2920	8 ABR17891	ABR17891 Aspergill
8	141.2	16.7	2987	8 ABR17891	ABR17891 Aspergill
9	141.2	15.6	1231	10 ABR84336	ABR84336 Aspergill
10	131.4	15.6	1231	10 ABR93057	ABR93057 Rice chor
11	131.4	15.6	1231	12 ADJ55263	ADJ55263 Rice chor
12	116.8	13.9	658	3 AAF14469	AAF14469 Aspergill
13	111.2	13.2	1223	10 ABR93056	ABR93056 Corn chor
14	111.2	12.4	1217	6 ABA91395	ABA91395 Corn chor
15	104.4	12.4	1217	6 ABA91395	ABA91395 Arabidops
16	104.4	11.8	1020	10 ABR93058	ABR93058 Soybean c
17	99.8	11.8	1020	12 ADJ55265	ADJ55265 Soybean c
18	97.4	11.6	798	6 ABZ13167	ABZ13167 Arabidops
19	97.4	11.6	993	6 ABA99614	ABA99614 Construct
20	97.4	11.6	993	6 ABA99614	ABA99614 Construct

21	97.4	11.6	1006	6 ABA99613	ABA99613 A. thalia
22	97.4	11.6	1006	6 ABA91400	ABA91400 Arabidops
23	97.4	11.6	1006	6 ABA91394	ABA91394 Arabidops
24	93.6	11.1	1005	6 ABZ12932	ABZ12932 Arabidops
25	93.6	11.1	1207	6 ABA91393	ABA91393 Arabidops
26	93.6	11.1	1207	6 ABA91399	ABA91399 Arabidops
27	93.6	11.1	1274	3 ACN53324	ACN53324 Arabidops
28	73	8.7	580	13 ACN57510	ACN57510 Cotton gy
29	69.8	8.3	622	13 ACN50132	ACN50132 Cotton no
30	64.2	7.6	600	13 ADR64815	ADR64815 Cotton CD
31	61.8	7.3	258	6 AB171526	AB171526 Corn taag
32	61	7.2	780	10 ABR93059	ABR93059 Wheat cho
33	61	7.2	780	12 ADJ55267	ADJ55267 Wheat cho
34	59.8	7.1	579	10 ABR93054	ABR93054 Wheat cho
35	59.8	7.1	579	12 ADJ55257	ADJ55257 Wheat cho
36	56.2	6.7	584	13 ACN50205	ACN50205 Cotton no
37	54.8	6.5	542	13 ACN57601	ACN57601 Cotton gy
38	53.4	6.3	525	10 ABR93053	ABR93053 Soybean c
39	53.4	6.3	525	12 ADJ55255	ADJ55255 Soybean c
40	52.6	6.2	524	13 ADR64235	ADR64235 Cotton CD
41	49.4	5.9	2000	8 ADA71938	ADA71938 Rice gene
42	48.8	5.8	864	12 ADU44958	ADU44958 Plant CDN
43	47.6	5.6	1379	8 ABA91794	ABA91794 Yeast mlt
44	47.6	5.6	5858	8 ADJ55726	ADJ55726 Nephtila m
45	46.8	5.6	180385	10 ADL13931	ADL13931 Ostreocarth

ALIGNMENTS

RESULT 1	
1 AAC81949	
ID AAC81949 standard; DNA; 843 BP.	
XX	
AC AAC81949;	
XX	
DT 15-SEP-2003 (revised)	
DT 01-MAR-2001 (first entry)	
XX	
DE H. polymorpha chorismate mutase DNA.	
XX	
KW Chorismate mutase; prephenate; selection marker; auxotrophic yeast; ds.	
XX	
OS Pichia angusta.	
XX	
PN WO200065071-A1.	
XX	
PD 02-NOV-2000.	
XX	
PF 27-APR-2000; 2000WO-BP003844.	
XX	
FR 27-APR-1999; 99DE-01019124.	
XX	
(RHRI-) RHEIN BIOTECH GRS NEUE BIOTECHNOLOGISCHE.	
DR Gellissen G, Braus G, Pries R, Krapmann S, Straesser AM;	
XX	
WPI: 2000-687355/67.	
XX	
P-PSDB; AAB11451.	
PT Nucleic acids encoding chorismate mutase, useful for preparing an	
XX	
PT auxotrophic selection system for recombinant yeast and for recombinant	
XX	
PS protein expression.	
XX	
Claim 1a; Page 57; 63pp; German.	
XX	
CC This invention describes novel nucleic acids (I) that encode a	
XX	
CC polypeptide (II) with chorismate mutase (CM) activity (or its	
XX	
CC complementary strand). CM catalyzes conversion of chorismate to	
XX	
CC prephenate, an essential precursor for Phe and Tyr. (I) is a selection	
XX	
CC marker for construction of corresponding auxotrophic yeast (requiring Phe	
XX	
CC and Tyr) that are used for recombinant production of proteins. (II) allows	
XX	
CC selection of transformed yeast on simple media. (Updated on 15-SEP-2003	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 19:49:03 ; Search time 634 Seconds
(without alignments)
8057.702 Million cell updates/sec

Title: US-10-042-059B-1

Perfect score: 843
Sequence: 1 atggacttaccgaagccaga.....tctctctgctgctgactag 843

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5615251 seqs, 303001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	100.0	843	US-10-042-059A-1	Sequence 1, Appli
2	843	100.0	1655	US-10-042-059A-3	Sequence 3, Appli
3	270	32.0	807	US-10-741-849-6032	Sequence 6032, Ap
4	156.4	18.6	869	US-10-472-587-26	Sequence 26, Appl
5	141.2	16.7	2920	US-10-128-714-249	Sequence 249, App
6	141.2	16.7	2987	US-10-128-714-249	Sequence 5249, App
7	131.4	15.6	1016	US-10-437-963-93956	Sequence 93956, A
8	131.4	15.6	1231	US-09-454-279-13	Sequence 13, Appl
9	131.4	15.6	1231	US-10-624-061-13	Sequence 13, Appl
10	118.2	14.0	1423	US-10-424-599-123820	Sequence 123820,
11	116.8	13.9	658	US-10-653-047-6992	Sequence 6992, Ap

12	116.6	13.8	1146	US-10-425-114-7285	Sequence 7285, Ap
13	116	13.8	1376	US-10-425-115-102347	Sequence 102347,
14	112.2	13.3	1548	US-10-739-930-4455	Sequence 4455, Ap
15	111.2	13.2	1223	US-09-454-279-11	Sequence 11, Appl
16	111.2	13.2	1223	US-10-624-061-11	Sequence 11, Appl
17	111.2	13.2	1500	US-10-767-701-14353	Sequence 14353, A
18	110.6	13.1	1010	US-10-425-115-102351	Sequence 102351,
19	109.6	13.0	1397	US-10-425-115-102346	Sequence 102346,
20	104.4	12.4	1217	US-10-267-763-4	Sequence 4, Appl1
21	104.4	12.4	1217	US-10-267-763-10	Sequence 10, Appl
22	103.2	12.2	1368	US-10-425-115-102349	Sequence 102349,
23	99.8	11.8	1020	US-09-454-279-15	Sequence 15, Appl
24	99.8	11.8	1020	US-10-624-061-15	Sequence 15, Appl
25	99.8	11.8	1079	US-10-425-114-7639	Sequence 7639, App
26	97.4	11.6	798	US-09-938-842A-972	Sequence 972, App
27	97.4	11.6	798	US-09-938-842A-972	Sequence 972, App
28	97.4	11.6	1006	US-10-267-763-3	Sequence 3, Appl1
29	97.4	11.6	1006	US-10-267-763-9	Sequence 9, Appl1
30	97	11.5	1430	US-10-739-930-4454	Sequence 4454, Ap
31	93.6	11.1	1005	US-09-938-842A-737	Sequence 737, App
32	93.6	11.1	1005	US-09-938-842A-737	Sequence 737, App
33	93.6	11.1	1207	US-10-267-763-2	Sequence 2, Appl1
34	93.6	11.1	1207	US-10-267-763-8	Sequence 8, Appl1
35	93.6	11.1	1299	US-10-739-930-621	Sequence 621, App
36	87.6	10.4	1653	US-10-424-599-93036	Sequence 93036, A
37	81	9.6	1197	US-10-425-114-3898	Sequence 3898, Ap
38	80	9.5	1314	US-10-425-115-151470	Sequence 151470,
39	78.4	9.3	1197	US-10-425-114-27576	Sequence 27576, A
40	77.2	9.2	524	US-10-425-115-102342	Sequence 102342,
41	76.2	9.0	768	US-10-437-963-49312	Sequence 49312, A
42	74.8	8.9	2154	US-10-437-963-83557	Sequence 83557, A
43	74.2	8.8	1066	US-10-425-114-13352	Sequence 13352, Ap
44	74.2	8.8	1083	US-10-425-115-115559	Sequence 115559,
45	73	8.7	580	US-10-021-923-12291	Sequence 12291, A

ALIGNMENTS

RESULT 1
US-10-042-059A-1
; Sequence 1, Application US/10042059A
; Publication No. US20020197704A1
; GENERAL INFORMATION:
; APPLICANT: Rhein Biotech Gesellschaft fur neue biotechnologische Prozesse und
; APPLICANT: Produktue mbH
; TITLE OF INVENTION: Nucleic Acid Molecule Containing a Nucleic Acid Coding for a Pol
; FILE REFERENCE: PA305805-019
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: DE 199 19 124.7
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 843
; TYPE: DNA
; ORGANISM: Haemulula polymorpha
US-10-042-059A-1

Query Match 100.0%; Score 843; DB 13; Length 843;
Best Local Similarity 100.0%; Pred. No. 6.4e-267;
Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C 1 ATGACCTTATGAAACCAAGAGTGTGACCTTGCAACATTAGAGATGCTGTC 60
D 1 ATGACCTTATGAAACCAAGAGTGTGACCTTGCAACATTAGAGATGCTGTC 60
C 61 CGAGTAGGAGATGATGATCATCTTCACTTATGAGAGGAGTGTGATGAGCGGCGCC 120
D 61 CGAGTAGGAGATGATGATCATCTTCACTTATGAGAGGAGTGTGATGAGCGGCGCC 120

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 19:31:58 ; Search time 3556 Seconds

(without alignments)
9023.672 Million cell updates/sec

Title: US-10-042-059B-1

Perfect score: 843
Sequence: 1 atgagactatgaagccagca.....ctctctcgtcgttactag 843

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_esc4:*
5: gb_esc5:*
6: gb_esc6:*
7: gb_esc7:*
8: gb_esc8:*
9: gb_esc9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	299	35.5	1185	9	CNS06T5P
2	176.6	20.9	937	9	CNS06T5P
3	176.6	20.9	1052	9	CNS06T5P
4	140	16.6	948	7	CO005472
5	137	16.3	574	8	BZ303243
6	132.8	15.8	738	7	CF877247
7	132.8	15.8	816	6	CB905545
8	125.4	14.9	788	7	CB905545
9	121.6	14.4	660	5	BX253798
10	116.8	13.9	798	6	CB619881
11	116.8	13.8	652	6	CD423256
12	113.8	13.5	747	9	CNS06T5P
13	113.2	13.4	710	7	CF475712
14	111.2	13.2	1222	7	AY103806
15	107.4	12.7	827	7	CO162332
16	106	12.6	988	7	ALJ83468
17	105.8	12.6	602	6	CD982471
18	105.8	12.5	903	7	CN149106
19	105.6	12.4	527	7	CO165812
20	104.6	12.4	606	4	BI995968
21	103	12.2	737	7	CO005473
22	103	12.2	867	6	CB619882
23	102.8	12.2	727	6	CA121888
24	102.2	12.1	680	6	CA080410

25	100.8	12.0	551	5	BQ701847
26	99.4	11.8	605	7	CN913779
27	98.6	11.7	607	8	BZ296833
28	98	11.6	495	1	AA786587
29	97.8	11.6	821	7	CK196770
30	97.4	11.6	837	7	CO366854
31	97	11.5	596	8	BZ296767
32	97	11.5	781	7	CF667838
33	96.6	11.5	853	7	CO366784
34	96.2	11.4	657	9	AG273371
35	96	11.4	812	7	CN148636
36	95	11.3	885	7	CV274873
37	94.8	11.2	857	7	CF635400
38	94.6	11.2	480	7	CV002646
39	94.4	11.2	707	6	CA239381
40	94.2	11.2	785	7	CNS23137
41	93.6	11.1	552	4	B1718858
42	93.6	11.1	1265	3	CNS046WL
43	93.6	11.1	1329	3	CNS04727
44	93.2	11.1	698	2	BE577489
45	93.2	11.1	830	6	CB622596

ALIGNMENTS

RESULT 1	CNS06T5P	1185 bp	DNA	linear	GSS 05-JUL-2001
LOCUS	T7 end of clone AW0AA029A11 of library AW0A from strain CL18 89 of				
DEFINITION	Yarrowia lipolytica, genomic survey sequence.				
ACCESSION	AL414131.1	GI:12186949			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Yarrowia lipolytica				
REFERENCE	Yarrowia lipolytica				
AUTHORS	Bukarjota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.				
	1 (bases 1 to 1185)				
	Soucier, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolochin-Fukuhara, M., Bon, E., Broctier, P., Casaregola, S., de-Montigny, J., Dujon, B., Duren, P., Lepingle, A., Liorette, B., Malpertuy, A., Neuvéglise, C., Ozier-Kalopoulou, O., Pottier, S., Saurin, M., Tekala, F., Toffano-Nicoche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.				
	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies				
	FBS Lett. 487 (1), 3-12 (2000)				
	2 (bases 1 to 1185)				
	Casaregola, S., Neuvéglise, C., Lepingle, A., Bon, E., Feynerol, C., Artiguenave, F., Wincker, P. and Galliard, C.				
	Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia lipolytica				
	FBS Lett. 487 (1), 95-100 (2000)				
	1152852				
	3 (bases 1 to 1185)				
	Genoscope.				
	Direct Submission				
	Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail: segre@genoscope.cns.fr - Web: www.genoscope.cns.fr)				
	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angustis, Debaryomyces hansenii var. hansenii, Pichia sorbitorphila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of				

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 21:57:48 / Search time 416 Seconds

(without alignments)
9924.137 Million cell updates/sec

Title: US-10-042-059b-1

Perfect score: 843
Sequence: 1 atgagcttcatgaagcaga.....tctctctcgcttctag 843

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	843	100.0	843 6	BD266599
2	843	100.0	843 6	BD266599
3	843	100.0	843 6	BD266599
4	843	100.0	843 6	BD266599
5	843	100.0	843 6	BD266599
6	843	100.0	843 6	BD266599
7	843	100.0	843 6	BD266599
8	843	100.0	843 6	BD266599
9	843	100.0	843 6	BD266599
10	843	100.0	843 6	BD266599
11	843	100.0	843 6	BD266599
12	843	100.0	843 6	BD266599
13	843	100.0	843 6	BD266599
14	843	100.0	843 6	BD266599
15	843	100.0	843 6	BD266599
16	843	100.0	843 6	BD266599
17	843	100.0	843 6	BD266599
18	843	100.0	843 6	BD266599
19	843	100.0	843 6	BD266599

20	2.4	1493	10	AF165986	AF165986 Mus muscu
21	2.4	2250	8	ATU09376	U09376 Arabidopsis
22	2.4	2479	10	BC029750	BC029750 Mus muscu
23	2.4	2479	6	C0849743	C0849743 Sequence
24	2.4	3873	9	AK126783	AK126783 Homo sapi
25	2.4	4149	9	BC041850	BC041850 Homo sapi
26	2.4	4322	8	AF486633	AF486633 Arabidops
27	2.4	10737	1	AB013312	AB013312 Methanosa
28	2.4	11287	1	AB011116	AB011116 Methanosa
29	2.4	38435	9	AC106801	AC106801 Homo sapi
30	2.4	95769	6	AX652128	AX652128 Sequence
31	2.4	95769	2	AC013430	AC013430 Genomic s
32	2.4	110000	8	AF006501.01	Continuation (2 of
33	2.4	110000	8	AC182132.35	Continuation (36 o
34	2.4	110000	8	AB016817.12	Continuation (13 o
35	2.4	118466	6	C0870115	C0870115 Sequence
36	2.4	124409	9	AC069360	AC069360 Homo sapi
37	2.4	131703	2	AC104642	AC104642 Trypanoso
38	2.4	150054	9	AL161901	AL161901 Human DNA
39	2.4	152593	8	AC002332	AC002332 Arabidops
40	2.4	154814	9	AC114802	AC114802 Homo sapi
41	2.4	156556	2	AC151236	AC151236 Bos tauru
42	2.4	167385	2	CR753906	CR753906 Dario rer
43	2.4	176580	10	AC127265	AC127265 Mus muscu
44	2.4	177623	10	AC138667	AC138667 Mus muscu
45	2.4	182032	2	AC150435	AC150435 Atelesrix
46	2.4	188006	2	AC147422	AC147422 Oryctolag
47	2.4	192634	2	AC069466	AC069466 Mus muscu
48	2.4	193614	10	AC110219	AC110219 Mus muscu
49	2.4	194045	10	AL833774	AL833774 Mouse DNA
50	2.4	208065	9	AC006676	AC006676 Homo sapi
51	2.4	208945	2	AC139756	AC139756 Mus muscu
52	2.4	210025	2	CR376847	CR376847 Dario rer
53	2.4	221610	2	AC134861	AC134861 Mus muscu
54	2.4	237933	2	AC111638	AC111638 Rattus no
55	2.4	239343	2	AC106481	AC106481 Rattus no
56	2.4	253961	2	AC128235	AC128235 Rattus no
57	2.4	254581	2	AC111674	AC111674 Rattus no
58	2.4	257570	2	CR354431	CR354431 Dario rer
59	2.4	257676	10	AL844852	AL844852 Mouse DNA
60	2.4	260692	2	AC134896	AC134896 Mus muscu
61	2.4	261934	5	BX664745	BX664745 Zebrafish
62	2.4	274676	1	AE017305	AE017305 Thermus t
63	2.4	295971	2	AC096027	AC096027 Rattus no
64	2.4	348672	1	CR378670	CR378670 Photobact
65	2.3	28	6	BD266604	BD266604 Nucleic a
66	2.3	51	6	C0001947	C0001947 Sequence
67	2.3	51	6	C0002131	C0002131 Sequence
68	2.3	243	4	PCMYO18	PCMYO18
69	2.3	261	4	RABMYVAS2	RABMYVAS2
70	2.3	261	4	RABMYVAS2	RABMYVAS2
71	2.3	344	6	AA462426	AA462426 Sequence
72	2.3	471	6	AX331324	AX331324 Sequence
73	2.3	471	6	AX331324	AX331324 Sequence
74	2.3	483	6	AX778298	AX778298 Sequence
75	2.3	575	10	OCOTARP	OCOTARP
76	2.3	687	6	AR491514	AR491514 Sequence
77	2.3	687	6	AR491514	AR491514 Sequence
78	2.3	702	4	S62056	S62056
79	2.3	751	11	BV041536	BV041536
80	2.3	775	9	HEA325303	HEA325303
81	2.3	870	6	BD211751	BD211751
82	2.3	954	9	AF026397	AF026397
83	2.3	1145	8	AK110798	AK110798
84	2.3	1166	9	BC007918	BC007918 Homo sapi
85	2.3	1176	3	BT011191	BT011191 Drosophi
86	2.3	1214	6	AA491513	AA491513 Sequence
87	2.3	1214	6	AX214360	AX214360 Sequence
88	2.3	1394	4	RABMYASAC	RABMYASAC
89	2.3	1514	9	HSU47925	HSU47925
90	2.3	1515	6	C0722412	C0722412 Sequence
91	2.3	1544	9	BC080585	BC080585 Homo sapi
92	2.3	1638	9	BC002353	BC002353 Homo sapi

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 9, 2005, 19:59:02 ; Search time 586 Seconds
(without alignments)
8515.942 Million cell updates/sec

Title: US-10-042-059B-1

Perfect score: 843
Sequence: 1 atcgacttatgaagccaga.....tctcctctgcttctgtag 843

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	100.0	843	3 AAC81949	Aac81949 H. polymo
2	843	100.0	1655	3 AAC81950	Aac81950 H. polymo
3	20	2.4	484	3 AAC37122	Aac37122 Arabidops
4	20	2.4	1044	13 ADS59363	ADS59363 Bacteri
5	20	2.4	1283	3 AAC47972	Aac47972 Arabidops
6	20	2.4	3873	13 ADRO6706	ADRO6706 Full leng
7	20	2.4	95769	8 ADA86859	ADA86859 Arabidops
8	20	2.4	118466	13 ABD32861	ABD32861 Human can
9	19	2.3	28	3 AAC81954	Aac81954 H. polymo
10	19	2.3	51	4 AAL27379	Aal27379 Human SNP
11	19	2.3	51	4 AAL27379	Aal27379 Human SNP
12	19	2.3	334	12 ADJ40487	Adj40487 Plant CDN
13	19	2.3	344	6 ABG92902	Abg92902 Tyriticum
14	19	2.3	369	6 AAL85587	Aal85587 Human pol
15	19	2.3	471	6 ABL63931	AbL63931 Breast ca
16	19	2.3	471	6 ABL63931	AbL63931 Breast ca
17	19	2.3	483	10 ADF79899	Adf79899 Leukaemia
18	19	2.3	507	13 ACN61244	ACN61244 Cotton gy
19	19	2.3	555	12 ADP29185	ADP29185 Human sec
20	19	2.3	565	13 ACN53545	ACN53545 Cotton an

21	19	2.3	589	12 ADL66198	ADL66198 DNA up-re
22	19	2.3	589	12 ADL66199	ADL66199 DNA up-re
23	19	2.3	676	12 ADJ42606	Adj42606 Plant CDN
24	19	2.3	870	3 AAZ57841	Aaz57841 Protein r
25	19	2.3	1214	5 AAS11360	Aas11360 Rice DNA
26	19	2.3	1514	13 ADR25630	ADR25630 Breast ca
27	19	2.3	1629	10 ADP70560	ADP70560 Orphan re
28	19	2.3	1767	12 ADO29954	ADO29954 Human GPC
29	19	2.3	1931	4 ABH06323	ABH06323 Drosophi
30	19	2.3	1980	4 ADS49231	ADS49231 Bacteri
31	19	2.3	2516	8 ABZ42526	ABZ42526 Human pro
32	19	2.3	2516	13 ADQ085304	ADQ085304 Human tum
33	19	2.3	2516	13 ADR25958	ADR25958 Breast ca
34	19	2.3	2890	13 ADH85116	ADH85116 Mouse ato
35	19	2.3	3219	11 ADM02536	ADM02536 Human CDN
36	19	2.3	3331	4 ABH06322	ABH06322 Drosophi
37	19	2.3	5661	2 AAV21518	Aav21518 Ratius no
38	19	2.3	5886	13 ADS97707	Ads97707 Rabbit al
39	19	2.3	5918	11 ACN924725	ACN924725 Breast ca
40	19	2.3	5925	12 ADP72935	ADP72935 Renal tox
41	19	2.3	5930	10 ADS52833	ADS52833 primary r
42	19	2.3	12801	13 ADS97709	Ads97709 Rabbid al
43	19	2.3	222930	6 ABR84349	ABR84349 Human CDN
44	18	2.1	309	6 ABR24499	ABR24499 Human ORP
45	18	2.1	333	5 AAF80051	AAF80051 Nucleotid
46	18	2.1	369	12 ADP93391	ADP93391 Cotton ex
47	18	2.1	405	9 ACH49258	Ach49258 Human leu
48	18	2.1	408	5 AAF80053	AAF80053 Nucleotid
49	18	2.1	537	13 ADR61828	ADR61828 Cotton CD
50	18	2.1	580	12 ACH69149	ACH69149 Human gen
51	18	2.1	586	13 ACN58170	ACN58170 Cotton gy
52	18	2.1	592	5 ADQ054235	ADQ054235 Novel can
53	18	2.1	732	3 AAS6702	Aas6702 DNA encod
54	18	2.1	741	12 ADI45730	ADI45730 Corn leop
55	18	2.1	741	12 ADJ44921	ADJ44921 Plant CDN
56	18	2.1	786	4 AAL02364	Aal02364 Human rep
57	18	2.1	804	13 ADS49193	ADS49193 Bacteri
58	18	2.1	808	5 AAF80052	AAF80052 Nucleotid
59	18	2.1	819	2 AAX99545	Aax99545 Nucleic a
60	18	2.1	897	5 AAF80050	AAF80050 Nucleotid
61	18	2.1	939	10 ADK54895	ADK54895 Plant DNA
62	18	2.1	954	13 ADS48734	ADS48734 Bacteri
63	18	2.1	1231	4 AAH344249	AAH344249 Human col
64	18	2.1	1434	3 AAC59740	AAC59740 Human sec
65	18	2.1	1434	8 ABZ73345	ABZ73345 Secreted
66	18	2.1	1434	8 ADA97947	Ada97947 Human sec
67	18	2.1	1434	8 ADA43853	Ada43853 Human sec
68	18	2.1	1434	10 ADC20102	ADC20102 Human sec
69	18	2.1	1434	10 ADP10566	ADP10566 Human sec
70	18	2.1	1434	10 ABZ66953	ABZ66953 Human sec
71	18	2.1	1458	4 AAC84376	AAC84376 Mouse CRD
72	18	2.1	1480	6 ABLJ39716	ABLJ39716 Human NS
73	18	2.1	1501	2 AAT09257	Aat09257 Human ara
74	18	2.1	1696	12 ADM47884	Adm47884 Polynucle
75	18	2.1	1904	12 ADM63411	ADM63411 Novel hum
76	18	2.1	1967	13 ADQ086139	ADQ086139 Human tum
77	18	2.1	2019	10 ADB62069	ADB62069 Human CDN
78	18	2.1	2020	6 AAS94898	Aas94898 Human DNA
79	18	2.1	2056	11 ACN90880	ACN90880 Breast ca
80	18	2.1	2088	13 ADS10128	ADS10128 Human the
81	18	2.1	2097	2 AAV26543	AAV26543 Human ret
82	18	2.1	2115	3 AAT96642	Aat96642 Human TYL
83	18	2.1	2115	3 AAN96943	Aan96943 Human TYL
84	18	2.1	2163	6 AEN96944	Aen96944 Gene #344
85	18	2.1	2163	9 ADB11525	ADB11525 Altiolococ
86	18	2.1	2278	9 ACA98960	ACA98960 CDNA enco
87	18	2.1	2404	13 ADRO6553	ADRO6553 Full leng
88	18	2.1	2420	4 ABL17625	ABL17625 Drosophi
89	18	2.1	2484	4 ABL03465	ABL03465 Drosophi
90	18	2.1	2540	5 AAF80049	AAF80049 Nucleotid
91	18	2.1	2856	5 AAF80048	AAF80048 Nucleotid
92	18	2.1			
93	18	2.1			

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 22:08:23 ; Search time 194 Seconds

(without alignments)
7110.213 Million cell updates/sec

Title: US-10-042-059b-1

Perfect score: 843

Sequence: 1 atggaacttatgaagcagca.....tctctctgctgctgctag 843

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents, NA:*

- 1: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
- 2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
- 3: /cgn2_6/prodata/1/lna/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/lna/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/lna/ECTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	2.4	98862	4 US-09-949-016-14133	Sequence 14133, A
2	20	2.4	102884	4 US-09-949-016-17100	Sequence 17100, A
3	19	2.3	687	4 US-09-780-717-30	Sequence 30, Appl
4	19	2.3	1214	4 US-09-780-717-28	Sequence 28, Appl
5	19	2.3	5661	3 US-08-938-105-2	Sequence 2, Appl
6	19	2.3	89210	4 US-09-949-016-16988	Sequence 16988, A
7	18	2.1	333	4 US-09-684-708A-8	Sequence 8, Appl
8	18	2.1	408	4 US-09-684-708A-12	Sequence 12, Appl
9	18	2.1	601	4 US-09-949-016-22999	Sequence 22999, A
10	18	2.1	601	4 US-09-949-016-23000	Sequence 23000, A
11	18	2.1	601	4 US-09-949-016-41205	Sequence 41205, A
12	18	2.1	601	4 US-09-949-016-41206	Sequence 41206, A
13	18	2.1	808	4 US-09-684-708A-10	Sequence 10, Appl
14	18	2.1	819	4 US-09-601-198-45	Sequence 45, Appl
15	18	2.1	819	4 US-09-270-767-10691	Sequence 10691, A
16	18	2.1	897	4 US-09-684-708A-6	Sequence 6, Appl
17	18	2.1	1581	4 US-09-949-016-243	Sequence 243, Appl
18	18	2.1	1588	4 US-09-949-016-1165	Sequence 1165, Ap
19	18	2.1	2115	3 US-09-032-365A-12	Sequence 12, Appl
20	18	2.1	2116	1 US-08-701-380-1	Sequence 1, Appl
21	18	2.1	2184	3 US-08-955-918C-1	Sequence 1, Appl
22	18	2.1	2184	3 US-08-697-766A-1	Sequence 1, Appl
23	18	2.1	2540	4 US-09-684-708A-4	Sequence 4, Appl
24	18	2.1	2856	4 US-09-684-708A-1	Sequence 1, Appl
25	18	2.1	8438	1 US-07-945-283-1	Sequence 1, Appl
26	18	2.1	8590	1 US-09-949-016-5562	Sequence 5562, Ap
27	18	2.1	10300	4 US-09-949-016-636	Sequence 636, Ap

28	18	2.1	25260	4 US-09-949-016-11985	Sequence 11985, A
29	18	2.1	25260	4 US-09-949-016-12907	Sequence 12907, A
30	18	2.1	34094	4 US-09-292-034-1	Sequence 1, Appl
31	18	2.1	38575	4 US-09-949-016-17304	Sequence 17304, A
32	18	2.1	57280	4 US-09-949-016-11796	Sequence 11796, A
33	18	2.1	57280	4 US-09-949-016-12843	Sequence 12843, A
34	18	2.1	57280	4 US-09-949-016-12844	Sequence 12844, A
35	18	2.1	57280	4 US-09-949-016-12846	Sequence 12846, A
36	18	2.1	57280	4 US-09-949-016-13542	Sequence 13542, A
37	18	2.1	57280	4 US-09-949-016-13543	Sequence 13543, A
38	18	2.1	57280	4 US-09-949-016-13544	Sequence 13544, A
39	18	2.1	57280	4 US-09-949-016-13545	Sequence 13545, A
40	18	2.1	57280	4 US-09-949-016-16633	Sequence 14633, A
41	18	2.1	57280	4 US-09-949-016-16634	Sequence 14634, A
42	18	2.1	57280	4 US-09-949-016-16635	Sequence 14635, A
43	18	2.1	57280	4 US-09-949-016-16636	Sequence 14636, A
44	18	2.1	57280	4 US-09-949-016-16637	Sequence 14637, A
45	18	2.1	57280	4 US-09-949-016-16638	Sequence 14638, A
46	18	2.1	57280	4 US-09-949-016-16639	Sequence 14639, A
47	18	2.1	57280	4 US-09-949-016-16640	Sequence 14640, A
48	18	2.1	119153	4 US-09-949-016-12378	Sequence 12378, A
49	18	2.1	285986	4 US-09-949-016-12287	Sequence 12287, A
50	18	2.1	288031	4 US-09-949-016-14864	Sequence 14864, A
51	18	2.1	4403765	3 US-09-103-840A-2	Sequence 2, Appl
52	18	2.1	4411529	3 US-09-103-840A-2	Sequence 1, Appl
53	17	2.0	278	4 US-09-640-211A-1368	Sequence 1368, Ap
54	17	2.0	288	4 US-09-252-991A-4801	Sequence 4801, Ap
55	17	2.0	562	4 US-09-668-751-224	Sequence 224, Ap
56	17	2.0	601	4 US-09-949-016-134896	Sequence 134896, A
57	17	2.0	601	4 US-09-949-016-134897	Sequence 134897, A
58	17	2.0	747	4 US-09-949-016-188364	Sequence 188364, A
59	17	2.0	747	3 US-08-750-145A-19	Sequence 19, Appl
60	17	2.0	747	3 US-08-975-698A-23	Sequence 23, Appl
61	17	2.0	747	3 US-09-417-090-23	Sequence 23, Appl
62	17	2.0	747	3 US-09-727-578-23	Sequence 23, Appl
63	17	2.0	940	2 US-08-713-000-3	Sequence 3, Appl
64	17	2.0	940	2 US-08-975-316-3	Sequence 3, Appl
65	17	2.0	940	3 US-09-211-710-3	Sequence 3, Appl
66	17	2.0	940	3 US-09-615-192A-3	Sequence 3, Appl
67	17	2.0	940	4 US-09-168-789-3	Sequence 3, Appl
68	17	2.0	1048	4 US-09-270-767-11465	Sequence 11465, A
69	17	2.0	1062	4 US-09-252-991A-3271	Sequence 3271, Ap
70	17	2.0	1098	4 US-09-902-540-3112	Sequence 3112, Ap
71	17	2.0	1144	4 US-09-640-211A-154	Sequence 154, Ap
72	17	2.0	1169	4 US-09-596-002-2	Sequence 2, Appl
73	17	2.0	1305	4 US-09-902-540-4277	Sequence 4277, Ap
74	17	2.0	1440	4 US-09-023-655-13399	Sequence 13399, Ap
75	17	2.0	1659	3 US-09-615-192A-124	Sequence 124, Ap
76	17	2.0	1659	4 US-09-169-789-124	Sequence 124, Ap
77	17	2.0	1672	4 US-09-949-016-2937	Sequence 2937, Ap
78	17	2.0	1785	2 US-08-975-316-48	Sequence 48, Appl
79	17	2.0	1785	3 US-09-615-192A-48	Sequence 48, Appl
80	17	2.0	1789	4 US-09-169-789-48	Sequence 48, Appl
81	17	2.0	3489	2 US-08-728-333A-1	Sequence 1, Appl
82	17	2.0	3489	2 US-09-298-568-1	Sequence 1, Appl
83	17	2.0	3489	4 US-09-410-399-1	Sequence 1, Appl
84	17	2.0	3489	4 US-09-894-273-1	Sequence 1, Appl
85	17	2.0	4251	4 US-09-902-540-536	Sequence 536, Ap
86	17	2.0	4692	2 US-08-916-917-1	Sequence 1, Appl
87	17	2.0	4692	2 US-08-972-631-1	Sequence 1, Appl
88	17	2.0	4692	2 US-08-972-629-1	Sequence 1, Appl
89	17	2.0	4692	2 US-08-972-630-1	Sequence 1, Appl
90	17	2.0	4692	2 US-08-672-211-1	Sequence 1, Appl
91	17	2.0	4692	3 US-09-225-170-1	Sequence 1, Appl
92	17	2.0	7014	4 US-09-949-016-15169	Sequence 15169, A
93	17	2.0	18809	4 US-09-902-540-1141	Sequence 1141, Ap
94	17	2.0	22294	4 US-09-949-016-15522	Sequence 15522, A
95	17	2.0	26012	4 US-09-902-540-1212	Sequence 1212, Ap
96	17	2.0	27630	2 US-09-949-016-12722	Sequence 12722, A
97	17	2.0	32207	2 US-08-770-379-20	Sequence 20, Appl
98	17	2.0	32207	3 US-08-757-669A-20	Sequence 20, Appl
99	17	2.0	32207	3 US-09-230-371A-20	Sequence 20, Appl
100	17	2.0	36138	4 US-08-311-731A-136	Sequence 136, Ap

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: April 9, 2005, 22:11:48 ; Search time 635 Seconds
(without alignments)
8045.012 Million cell updates/sec

Title: US-10-042-059B-1

Perfect score: 843
Sequence: 1 atggaacttatgaaccaga.....tctctctgcttctag 843

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 5615251 seqs, 3030001701 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	100.0	843	US-10-042-059A-1	Sequence 1, Appli
2	843	100.0	1655	US-10-047-059A-3	Sequence 3, Appli
3	22	2.6	1936	US-10-424-589-58517	Sequence 58517, A
4	20	2.4	1044	US-10-369-493-35037	Sequence 35037, A
5	20	2.4	1309	US-10-425-114-23242	Sequence 23242, A
6	19	2.3	334	US-10-260-238-1487	Sequence 1487, Ap
7	19	2.3	471	US-09-954-531-766	Sequence 766, App
8	19	2.3	471	US-09-954-531-1201	Sequence 1201, Ap
9	19	2.3	471	US-10-843-641A-1833	Sequence 1833, Ap
10	19	2.3	471	US-10-843-641A-2268	Sequence 2268, Ap
11	19	2.3	507	US-10-021-333-16025	Sequence 16025, A

12	19	2.3	565	US-10-021-323-8326	Sequence 8326, Ap
13	19	2.3	589	US-10-430-201-2591	Sequence 2591, Ap
14	19	2.3	589	US-10-430-201-2592	Sequence 2592, Ap
15	19	2.3	676	US-10-260-238-3606	Sequence 3606, Ap
16	19	2.3	687	US-09-780-717-30	Sequence 30, Appli
17	19	2.3	1214	US-09-780-717-28	Sequence 28, Appli
18	19	2.3	1514	US-10-172-118-1491	Sequence 1491, Ap
19	19	2.3	1514	US-10-342-887-1491	Sequence 1491, Ap
20	19	2.3	1786	US-10-738-930-5058	Sequence 5058, Ap
21	19	2.3	1980	US-10-369-493-37661	Sequence 37661, A
22	19	2.3	2069	US-10-437-963-32618	Sequence 32618, A
23	19	2.3	2516	US-10-225-567A-533	Sequence 533, App
24	19	2.3	2516	US-10-172-118-1819	Sequence 1819, Ap
25	19	2.3	3219	US-10-342-887-1819	Sequence 1819, Ap
26	19	2.3	3219	US-10-108-260A-1221	Sequence 1221, Ap
27	19	2.3	5886	US-10-798-037-3	Sequence 3, Appli
28	19	2.3	5918	US-10-198-846-13875	Sequence 13875, A
29	19	2.3	5925	US-10-191-803-104	Sequence 104, App
30	19	2.3	12801	US-10-798-037-5	Sequence 5, Appli
31	19	2.3	23810	US-10-741-600-17925	Sequence 17925, A
32	18	2.1	25	US-10-098-263B-61325	Sequence 61325, A
33	18	2.1	231	US-10-242-555A-4564	Sequence 4564, Ap
34	18	2.1	231	US-10-085-783A-4564	Sequence 4564, Ap
35	18	2.1	247	US-10-425-115-24483	Sequence 94483, A
36	18	2.1	315	US-10-437-963-10812	Sequence 10812, A
37	18	2.1	337	US-10-425-114-22093	Sequence 22093, A
38	18	2.1	360	US-10-425-115-171112	Sequence 171112, A
39	18	2.1	369	US-09-732-627A-2402	Sequence 2402, Ap
40	18	2.1	405	US-09-918-995-36470	Sequence 36470, A
41	18	2.1	432	US-10-437-963-39613	Sequence 39613, A
42	18	2.1	471	US-10-437-963-16623	Sequence 16623, A
43	18	2.1	505	US-10-425-115-83642	Sequence 93642, A
44	18	2.1	537	US-10-767-795-2609	Sequence 2609, App
45	18	2.1	586	US-10-029-386-2344	Sequence 2344, Ap
46	18	2.1	586	US-10-021-323-12951	Sequence 12951, A
47	18	2.1	599	US-10-767-701-24405	Sequence 24405, A
48	18	2.1	634	US-10-425-115-13403	Sequence 13403, A
49	18	2.1	642	US-10-437-963-82559	Sequence 82559, A
50	18	2.1	665	US-10-425-115-7244	Sequence 7244, Ap
51	18	2.1	682	US-10-425-115-78516	Sequence 78516, A
52	18	2.1	741	US-10-259-194A-661	Sequence 661, App
53	18	2.1	741	US-10-260-238-5921	Sequence 5921, App
54	18	2.1	785	US-10-437-963-68399	Sequence 68399, A
55	18	2.1	786	US-09-764-891-2365	Sequence 2365, App
56	18	2.1	804	US-10-369-493-27623	Sequence 27623, A
57	18	2.1	819	US-10-349-680-139	Sequence 139, App
58	18	2.1	822	US-10-156-761-344	Sequence 344, App
59	18	2.1	954	US-10-369-493-27164	Sequence 27164, A
60	18	2.1	999	US-10-425-115-55402	Sequence 55402, A
61	18	2.1	1068	US-10-437-963-44305	Sequence 44305, A
62	18	2.1	1128	US-10-156-761-2338	Sequence 2338, App
63	18	2.1	1231	US-10-106-698-1341	Sequence 1341, Ap
64	18	2.1	1348	US-10-437-963-40676	Sequence 40676, A
65	18	2.1	1545	US-10-425-114-33927	Sequence 33927, A
66	18	2.1	1640	US-10-425-115-7248	Sequence 7248, Ap
67	18	2.1	1683	US-10-424-599-13751	Sequence 13751, A
68	18	2.1	1689	US-10-425-115-55404	Sequence 55404, A
69	18	2.1	1696	US-10-310-154-302	Sequence 302, App
70	18	2.1	1774	US-10-437-963-94064	Sequence 94064, A
71	18	2.1	1952	US-10-767-701-12942	Sequence 12942, A
72	18	2.1	2019	US-10-104-047-223	Sequence 223, App
73	18	2.1	2020	US-10-240-965-153	Sequence 153, App
74	18	2.1	2056	US-10-198-846-12030	Sequence 12030, A
75	18	2.1	2116	US-09-880-107-3441	Sequence 3441, Ap
76	18	2.1	2145	US-10-437-963-40675	Sequence 40675, A
77	18	2.1	2217	US-10-437-963-40678	Sequence 40678, A
78	18	2.1	2745	US-10-027-632-112242	Sequence 112242, A
79	18	2.1	2745	US-10-027-632-112242	Sequence 112242, A
80	18	2.1	2745	US-10-027-632-112242	Sequence 63297, A
81	18	2.1	2912	US-10-437-963-68397	Sequence 68397, A
82	18	2.1	3190	US-10-108-260A-2319	Sequence 2319, Ap
83	18	2.1	4370	US-09-764-891-9644	Sequence 9644, Ap
84	18	2.1	6822	US-10-425-115-129369	Sequence 129369, A
85	18	2.1	10300	US-09-960-253-145	Sequence 145, App

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 20:58:23 / Search time 3558 Seconds
(without alignments)
9018.600 Million cell updates/sec

Title: US-10-042-059b-1

Perfect score: 843
Sequence: 1 atgagcttattcgaagccaga.....tctcctctgcttctag 843

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

EST:
1: gb_esc1:*
2: gb_esc2:*
3: gb_hic:*
4: gb_esc3:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_gsa1:*
9: gb_gsa2:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2.8	567	6	CB456917	CB456917 714231 MA
2	2.7	615	7	CO889914	CO889914 Bovgen.18
3	2.7	781	5	BX881595	BX881595 BX881595
4	2.6	246	6	AW705733	AW705733 BK51B05.Y
5	2.6	279	7	CK124266	CK124266 BES182410
6	2.6	319	1	AI959790	AI959790 sc94B09.Y
7	2.6	443	4	BM309799	BM309799 bak6605.Y
8	2.6	573	6	CD402848	CD402848 Gm CK2544
9	2.6	601	2	BP258490	BP258490 HVSMEF001
10	2.6	626	2	BE661641	BE661641 2-G11 Gma
11	2.6	657	4	BI958372	BI958372 HVSMEH001
12	2.6	662	4	AW349601	AW349601 GM210005A
13	2.6	1093	9	CN607768	AL432294 T7 end of c
14	2.5	63	9	CR068930	Forward s
15	2.5	233	2	BP911142	BP911142 PM1-UT006
16	2.5	247	2	BP909761	BP909761 PM1-UT006
17	2.5	263	2	BP910260	BP910260 PM1-UT006
18	2.5	263	2	AW477877	AW477877 17402 MAR
19	2.5	441	6	CB931218	CB931218 r15409.Y
20	2.5	488	8	BZ302958	BZ302958 KD2125.G1
21	2.5	496	2	BP074380	BP074380 221782 MA
22	2.5	496	6	CB455541	CB455541 712687 MA
23	2.5	540	2	BE012467	BE012467 121924 MA
24	2.5	549	4	BI359976	BI359976 384767 MA

25	2.5	563	5	B0119118	B0119118 EST604694
26	2.5	587	1	BK665191	BK665191 BX665191
27	2.5	593	7	CK838080	CK838080 4063604 B
28	2.5	656	1	AU296144	AU296144 AU296144
29	2.5	660	5	BK602109	BK602109 BX602109
30	2.5	819	4	BI407957	BI407957 602918731
31	2.5	821	5	BP463227	BP463227 BP463227
32	2.5	844	5	BP170445	BP170445 BP170445
33	2.5	853	9	CR143596	CR143596 Reverse s
34	2.5	884	9	CNS0398A	AL452172 T. brucei
35	2.5	937	2	BF122575	BF122575 Tetradon
36	2.5	1033	5	BQ894385	BQ894385 AGENCOURT
37	2.5	269	5	BP100096	BP100096 BP100096
38	2.4	273	4	BP952290	BG952290 CM4-CT062
39	2.4	284	9	TA12H03P	TA12H03P T. brucei
40	2.4	321	8	B27554	B27554 P20H3TRB IG
41	2.4	345	4	BU609946	BU609946 BU609946
42	2.4	350	1	AV524543	AV524543 AV524543
43	2.4	360	9	BX894982	BX894982 Arabidops
44	2.4	415	4	BI691463	BI691463 603310916
45	2.4	429	8	B27297	B27297 F2E3TR IG
46	2.4	449	2	BE809494	BE809494 215061 MA
47	2.4	471	7	CN104206	CN104206 EC2CA25B
48	2.4	489	8	BH230880	BH230880 1006159H0
49	2.4	493	1	AV441702	AV441702 AV441702
50	2.4	521	6	CB186427	CB186427 TgESTYF2
51	2.4	526	6	CB259248	CB259248 68-E01117
52	2.4	528	7	CN251799	CN251799 EST017730
53	2.4	542	1	AV554615	AV554615 CH240_426
54	2.4	544	1	AV554612	AV554612 AV554612
55	2.4	549	8	AZ833646	AZ833646 2M0115C23
56	2.4	562	7	CF811383	CF811383 NA413 CDN
57	2.4	581	6	CD217095	CD217095 TgESTYF12
58	2.4	610	4	BJ607944	BJ607944 BJ607944
59	2.4	613	8	AZ998423	AZ998423 2M0285B23
60	2.4	621	5	BQ826796	BQ826796 g47C04.x
61	2.4	621	7	CN253182	CN253182 EST019121
62	2.4	627	4	BI159482	BI159482 602920296
63	2.4	643	4	BJ606766	BJ606766 BJ606766
64	2.4	656	7	CK118964	CK118964 215618.D1
65	2.4	658	1	AV822322	AV822322 AV822322
66	2.4	659	5	BX924334	BX924334 BX924334
67	2.4	660	6	CB469076	CB469076 sn02_H02.
68	2.4	669	5	BX919629	BX919629 BX919629
69	2.4	670	8	AZ310918	AZ310918 1M0026A11
70	2.4	688	4	BJ591286	BJ591286 BJ591286
71	2.4	693	4	BI150046	BI150046 602849459
72	2.4	696	2	BE038046	BE038046 AA08B12 A
73	2.4	715	9	AC9391581	AC9391581 Mus muscu
74	2.4	724	4	BI105542	BI105542 602891878
75	2.4	734	4	BI460985	BI460985 603304633
76	2.4	752	4	BI111057	BI111057 602899694
77	2.4	760	9	CL159077	CL159077 104_348.1
78	2.4	764	4	BI686089	BI686089 603313070
79	2.4	763	4	BI663982	BI663982 603388652
80	2.4	773	7	CO001622	CO001622 EST789957
81	2.4	770	4	BI455983	BI455983 603317161
82	2.4	776	2	BI155993	BI155993 602903527
83	2.4	796	2	BF163092	BF163092 601769608
84	2.4	806	4	BG918558	BG918558 602818331
85	2.4	806	5	BU057678	BU057678 UI-M-FRO-
86	2.4	806	5	BX920432	BX920432 BX920432
87	2.4	841	8	BZ755150	BZ755150 PUDH04TB
88	2.4	846	8	BZ799633	BZ799633 PUFV79TD
89	2.4	859	4	BG919233	BG919233 602818064
90	2.4	865	4	BI661415	BI661415 603304708
91	2.4	875	9	CNS048B2	AL479188 Tetradon
92	2.4	886	7	CO001683	CO001683 EST990018
93	2.4	890	4	BI686188	BI686188 603313186
94	2.4	890	4	BI854697	BI854697 603381637
95	2.4	892	7	CO001682	CO001682 EST790017
96	2.4	892	8	BZ799630	BZ799630 PUFV79TB
97	2.4	917	4	BI663623	BI663623 603388331